

Serial No.: 10/552,857
Response to Office Action mailed: January 6, 2011
Amendment Dated: April 18, 2011

REMARKS/ARGUMENTS

This is in response to the Office Action mailed January 6, 2011 for the above-captioned application.

Applicants request and extension of time sufficient to make this paper timely and enclose the fee.

Claims 65-73 and 75-82 have been cancelled without prejudice, and new claims 83-102 have been added. The presentation of these claims is consistent with the remarks made by the examiner in the office action, and clarifying comments made in the telephone interview on January 5, 2011. This paper will serve as Applicants summary of that telephone interview.

In the claims, consistent with the office action (Page 3), references to "BANYULS" have been replaced with "anthocyanidine reductase." In addition, the claims have been divided into two groups as suggested by the Examiner in the interview. Claims 83-97 are directed to constructs that increase the amounts of the recited proteins and the use of constructs. Claims 98 to 102 are directed to constructs that decrease the amount of the recited proteins.

Specifically, new claim 83 refers to a nucleic acid construct that includes at least two portions: a first nucleic acid portion encoding a chalcone synthase and a second nucleic acid portion encoding an anthocyanidine reductase. Specific sequences and variants with at least 95% identity are listed in the claim, and the claim further recites that the construct increases the levels of both CHS and anthocyanidine reductase when introduced into a plant. This claims is believed to be free of the rejections of record.

The prior claims were rejected under 35 USC § 112, first and second paragraphs. This claim does not include reference to BANYULS, but rather to anthocyanidine reductase which has a clear function to link to the functionally active variants. Further, this claims does not contain a reference to fragments so the issue regarding relative short (60 base) fragments not encoding enough amino acids to provide functional protein activity is overcome.

In new claim 83, both the elected sequences, and the non-elected sequences have been maintained. Applicants submit that the various sequences for the nucleotides and proteins can be used interchangeably for the stated functions and that in the absence of art teaching or suggesting the parts of the construct by function, patentability does not depend on the specific sequence, and that constructs for the same purpose should not be treated as different inventions, but rather as species. Further, Applicants note the examiners's comments concerning the similarity of Seq ID Nos. 12, 14 and 16. Each of these sequences is within the variation limit and thus separate claims (in separate applications) to the sequences would result in claims with

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overlapping scope that could not be addressed through a double patenting rejection because of the restriction requirement. This would seem to be undesirable from a public policy perspective. On the other hand, a truly generic claim that does not recite the specific sequences disclosed could run afoul of written description issues, and therefore is not be submitted at this time to avoid delay in receiving a Notice of Allowance. Claim 89 is added specific to the elected sequences. Claim 90 is comparable to coding portions of prior claim 81 which was indicated to be allowable if rewritten to independent form.

New claim 98 is directed to a construct for reducing the amount of the recited proteins. As the examiner acknowledged in the interview this can be accomplished by antisense mechanisms or through sense suppression mechanisms, and fragments are used for decreasing the amount of a protein. Thus this claim refers to both the sense sequences and the complements thereof, variants thereof, and fragments. Since the claim recites a decrease in protein amounts, this is the meaning of the "functionally active" language in this claim.

With this amendment, the present application is believed to be in form for allowance. Further, consideration of the non-elected sequences, all of which have similarity in both structure and function within the relevant group, as reflected in the alignments previously submitted is respectfully urged.

Respectfully submitted,



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